

## IN THE CLAIMS

Claims 14 and 19-23 are amended. The claims are reproduced below.

1.- 13. (Cancelled)

14. (Currently amended) A computer-implemented method of generating a local-global alignment score which that indicates a global and a local similarity between a first protein structure and a second protein structure, the method executed by ~~one or more computer systems~~ a computer system and comprising:

receiving, at the ~~one or more computer systems~~ computer system, a protein structure correspondence ~~wherein a plurality of positions in the protein structure~~  
~~correspondence indicates~~ having a plurality of positions indicating a corresponding pair of residues in the first protein structure and the second protein structure;  
~~the one or more computer systems~~ determining, by the computer system and according to  
a plurality of specified threshold values, a plurality of root mean square deviations corresponding to a plurality of sets of pairs of residues, ~~wherein each set of pairs of residues comprises~~ including a plurality of pairs of residues that are contiguous in the protein structure correspondences, ~~and the plurality of root mean square deviations are determined using a plurality of specified threshold values;~~  
~~the one or more computer systems~~ selecting, by the computer system, a longest contiguous segment corresponding to a set of pairs of residues of the plurality of pairs of residues based on the plurality of root mean square deviations;  
determining, by the computer system, a global distance test value based on a plurality of distance scores, each score corresponding to a number of pairs of residues in the correspondence within a pre-defined distance of a plurality of pre-defined distances;  
~~the one or more computer systems~~ identifying a plurality of distance scores, wherein each distance score corresponds to a number of pairs of residues in the correspondence that

are within a pre-defined distance of a plurality of pre-defined distances  
the one or more computer systems selecting a global distance test value based on the  
plurality of distance scores;—  
the one or more computer systems generating, by the computer system, the local-global  
alignment score based on the longest contiguous segment and the global distance test  
value; and  
the one or more computer systems providing, by the computer system, a result based on  
the local-global alignment score.

15.-18. (Cancelled)

19. (Currently amended) The method of claim 14, wherein the ~~one or more~~  
computer systems ~~comprise~~ system includes a server and the method further ~~comprising~~  
comprises:

receiving, at [[a]] the server, a first set of co-ordinates associated with the first protein  
structure from a client;  
receiving, at the server, a second set of co-ordinates associated with the second protein  
structure; and  
the server generating the protein structure correspondence based on the first set of co-  
ordinates and the second set of co-ordinates.

20. (Currently amended) The method of claim 14, further comprising:  
receiving, at the one or more computer systems computer system, a first set of co-  
ordinates associated with the first protein structure;  
receiving, at the one or more computer systems computer system, a second set of co-  
ordinates associated with the second protein structure; and  
the one or more computer systems generating, by the computer system, the protein

structure correspondence based on the first set of co-ordinates and the second set of co-ordinates.

21. (Currently amended) The method of claim 20, wherein providing a result based on the local-global alignment score further comprises:

~~the one or more computer systems~~ generating, by the computer system, a second protein structure correspondence based on the local-global alignment score; and  
~~the one or more computer systems~~ providing, by the computer system, the second protein structure correspondence.

22. (Currently amended) The method of claim 20, wherein providing the second protein structure correspondence comprises:

~~the one or more computer systems~~ computer system modifying the set of co-ordinates specifying the first protein structure based on at least one of the global distance test value and the longest continuous segment to generate a second set of co-ordinates specifying the first protein structure; and  
~~the one or more computer systems~~ computer system providing the second set of co-ordinates.

23. (Currently amended) The method of claim 21, wherein providing the second protein structure correspondence comprises:

~~the one or more computer systems~~ computer system displaying a graphical representation of at least one of the first protein structure or the second protein structure, wherein at least some of the residues in the graphical representation are colored according to distance between the at least some of the residues and the corresponding residues in the second protein structure.

24. (Previously Presented) The method of claim 23, wherein the graphical representation is a bar plot.

25. (Previously Presented) The method of claim 23, wherein the graphical representation is a three-dimensional protein structure.